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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/506,078DATE: 03/08/2000  
TIME: 15:24:39

Input Set: I506078.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

p.5

ENTERED

1 <110> APPLICANT: Pfizer Products Inc  
2 <120> TITLE OF INVENTION: FUSION PROTEINS COMPRISING CARRIERS THAT CAN INDUCE A  
3 DUAL IMMUNE RESPONSE  
4 <130> FILE REFERENCE: PC10202A  
5 <140> CURRENT APPLICATION NUMBER: US/09/506,078  
6 <141> CURRENT FILING DATE: 2000-02-16  
7 <150> EARLIER APPLICATION NUMBER: N/A  
8 <151> EARLIER FILING DATE: 1999-02-17  
9 <160> NUMBER OF SEQ ID NOS: 46  
10 <170> SOFTWARE: PatentIn Ver. 2.1  
11 <210> SEQ ID NO 1  
12 <211> LENGTH: 33  
13 <212> TYPE: DNA  
14 <213> ORGANISM: Artificial Sequence  
15 <220> FEATURE:  
16 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
17 OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE  
18 AND CLONING ENDS  
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20 catggaacac tgggtcttatg gtctgcgtcc ggg 33  
21 <210> SEQ ID NO 2  
22 <211> LENGTH: 33  
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24 <213> ORGANISM: Artificial Sequence  
25 <220> FEATURE:  
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28 AND CLONING ENDS  
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31 <210> SEQ ID NO 3  
32 <211> LENGTH: 36  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Artificial Sequence  
35 <220> FEATURE:  
36 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
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38 AND CLONING ENDS  
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40 gatctggaac actggtctta tgggtctgcgt ccgggc 36  
41 <210> SEQ ID NO 4  
42 <211> LENGTH: 36  
43 <212> TYPE: DNA  
44 <213> ORGANISM: Artificial Sequence

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45 <220> FEATURE:
46 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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48 AND CLONING ENDS
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50 gatcgcccgg acgcagacca taagaccagt gttcca 36
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52 <211> LENGTH: 76
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
57 OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
58 AND CLONING ENDS
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60 gatccatgga gcactgggtca tatggtctgc gtccgggtga acattggagc tacggtctac 60
61 gccccgggtc catggc 76
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63 <211> LENGTH: 76
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67 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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69 AND CLONING ENDS
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71 tcgagccatg gacccggggc gtagaccgta gtcctaatgt tcacccggac gcagaccata 60
72 tgaccagtgc tccatg 76
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78 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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81 <400> SEQUENCE: 7
82 ggggaacact ggtcttatgg cttacggccg ggagagcatt ggagttacgg cctccgtcca 60
83 ggttccatgg c 71
84 <210> SEQ ID NO 8
85 <211> LENGTH: 75
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
89 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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91 AND CLONING ENDS
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93 tcgagccatg gaacctggac ggaggccgta actccaatgc tctcccgcc gtaagccata 60
94 agaccagtgt tcccc 75

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102     AND CLONING ENDS
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104     gatccagagc actggtcata tggctcgcgt ccgggtgaac attggagcta cggtctacgc 60
105     cccggggatc c                                     71
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109 <213> ORGANISM: Artificial Sequence
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111 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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115     tcgaggatcc ccggggcgta gaccgtagct ccaatgttca cccggacgca gaccatatga 60
116     ccagtgtctt g                                     71
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125 <400> SEQUENCE: 11
126     ggggaacact ggtcttatgg cttacggccg ggagagcatt ggagttacgg cctccgtcca 60
127     ggggatcc                                         68
128 <210> SEQ ID NO 12
129 <211> LENGTH: 72
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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135     AND CLONING ENDS
136 <400> SEQUENCE: 12
137     tcgaggatcc cctggacgga ggccgtaact ccaatgtctt cccggccgta agccataaga 60
138     ccagtgttcc cc                                     72
139 <210> SEQ ID NO 13
140 <211> LENGTH: 10
141 <212> TYPE: PRT
142 <213> ORGANISM: GNRH AMINO ACID SEQUENCE
143 <400> SEQUENCE: 13
144     Glu His Trp Ser Tyr Gly Leu Arg Pro Gly

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145          1          5          10
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147 <211> LENGTH: 328
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence: part of
152 plasmid p9897-R
153 <400> SEQUENCE: 14
154   acgccagggt tttcccagtc acgacgttgt aaaacgacgg ccagtgagcg cgcgtaatac 60
155   gactcactat agggcgaatt ggagctccac cgcggtggcg gccgctctag aactagtgga 120
156   tccagagcac tggtcataat gctcgcgtcc gggatgaacat tggagctacg gtctacgccc 180
157   cggggaacac tggctcttat gcttacggcc gggagagcat tggagttacg gcctccgtcc 240
158   aggttccatg ggctcgaggg ggggcccggg acccagcttt tgttcccttt agtgagggtt 300
159   aattgcgcgc ttggcgtaat atggtcat                               328
160 <210> SEQ ID NO 15
161 <211> LENGTH: 40
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Description of Artificial Sequence: GnRH tetramer
166 <400> SEQUENCE: 15
167   Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly
168       1          5          10          15
169   Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His
170           20          25          30
171   Trp Ser Tyr Gly Leu Arg Pro Gly
172           35          40
173 <210> SEQ ID NO 16
174 <211> LENGTH: 1259
175 <212> TYPE: DNA
176 <213> ORGANISM: Bovine herpesvirus 1
177 <220> FEATURE:
178 <221> NAME/KEY: gene
179 <222> LOCATION: (1)..(1259)
180 <223> OTHER INFORMATION: sequence encoding BHV-1 gD from clone
181 FlgD/Pots207(#79)
182 <400> SEQUENCE: 16
183   ccatggaggg gccgacattg gccgtgctgg gcgcgctgct cgcggttgcg gtaagcttgc 60
184   ctacacccgc gccgcgggtg acggtatacg tcgaccgcgc gccgtaccgc atgccgcgat 120
185   acaactacac tgaacgctgg cacactaccg ggccataacc gtcgcccttc gcagacggcc 180
186   gcgagcagcc cgtcgagggt cgctacgcga cgagcgcggc gccgtgcgac atgctggcgc 240
187   tgatcgcaga cccgcagggt gggcgcacgc tgtgggaagc ggtacgccgg cagcgcgcgc 300
188   cgtacaacgc caccggtcat tggtaacaag tcgagagcgg gtgcgcccgc gtactgtact 360
189   acatggagta caccgagtg cagcccagga agcactttgg gtactgccgc taccgcacac 420
190   ccccgctttg ggacagcttc ctggcgggct tcgcctaccc caccgacgac gagctgggac 480
191   tgattatggc ggcgcccgcg cggctcgtcg agggccagta ccgacgcgcg ctgtacatcg 540
192   acggcacggg gcctataca gatctcatgg ttctcgtgcc ggccggggac tgctggttct 600
193   cgaaactcgg cgcggctcgc gggtacacct ttggcgcgtg cttcccggcc cgggattacg 660
194   agcaaaagaa ggttctgcgc ctgacgtatc tcacgcagta ctaccgcgag gaggcacaca 720

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195      aggccatagt cgactactgg ttcattgcgcc acggggggcgt cgttccgcgcg tattttgagg 780
196      agtcgaaggg ctacgagccg ccgcctgccg ccgatggggg ttccccgcgcg ccaccgcgcg 840
197      acgacgaggg ccgcgaggat gaaggggaga ccgaggacgg ggcagccggg cgggagggca 900
198      acggcggccc cccaggaccc gaaggcgacg gcgagagtca gacccccgaa gccaacggag 960
199      gcgccgaggg cgagccgaaa cccggcccca gcccgcagcg cgaccgcccc gaaggctggc 1020
200      cgagcctcga agccatcacg cccccccgcg ccgccccgcg tacgcccgcg cgagctccgg 1080
201      acgctgtttc ggtttctggt ggtatcggtg tcgctgctgc tgctatcgct tgcgttgctg 1140
202      ctgctgctgc tgggtgcttac ttcgtttata ttcgctgctg tgggtgctggc ccgctgcccg 1200
203      gtaaaccgaa aaaactgccg gctttcggtg acgttaacta cagtgtctcg ccgggttga 1259

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204 &lt;210&gt; SEQ ID NO 17

205 &lt;211&gt; LENGTH: 418

206 &lt;212&gt; TYPE: PRT

207 &lt;213&gt; ORGANISM: Bovine herpesvirus 1

208 &lt;220&gt; FEATURE:

209 &lt;221&gt; NAME/KEY: PEPTIDE

210 &lt;222&gt; LOCATION: (1)..(418)

211 &lt;223&gt; OTHER INFORMATION: BHV-1gD encoded by clone FlgD/Pots207nco(#79)

212 &lt;400&gt; SEQUENCE: 17

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213      Met Glu Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ala
214      1              5              10              15
215      Val Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro
216      20              25              30
217      Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr
218      35              40              45
219      Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val
220      50              55              60
221      Glu Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu
222      65              70              75              80
223      Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg
224      85              90              95
225      His Ala Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser
226      100             105             110
227      Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro
228      115             120             125
229      Arg Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Phe Trp Asp
230      130             135             140
231      Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu
232      145             150             155             160
233      Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala
234      165             170             175
235      Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu
236      180             185             190
237      Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr
238      195             200             205
239      Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val
240      210             215             220
241      Leu Arg Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys
242      225             230             235             240
243      Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro
244      245             250             255

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Please Note:

Please ensure that all subsequent artificial/unknown sequences have a suitable explanation in the  
<220> - <223> section.

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**VERIFICATION SUMMARY**  
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Line ? Error/Warning

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